

Amendments to the Claims:

The following Listing of Claims will replace all prior versions, and listings, of the claims in the above-identified application.

Listing of Claims

1. (currently amended) An isolated and purified-poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) ~~or a functional equivalent thereof which is at least 95% homologous to~~ or a PARP homolog with at least 85% identity with human PARP2 (SEQ ID NO: 2), which exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which
 - a) has a functional NAD⁺ binding domain comprising the sequence
PX_n(S/T)GX₃GKGIYFA (SEQ ID NO:11)
in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;
 - and
 - b) lacks a zinc finger sequence of the formula
CX₂CX_mHX₂C (SEQ ID NO:30)
in which m is an integral value of 28 or 30, and the X radicals are, independently of one another, any amino acid.
2. (previously presented) The PARP homolog as claimed in claim 1, wherein the functional NAD⁺ binding domain comprises the following sequence:
(S/T)XGLR(I/V)XPX_n(S/T)GX₃GKGIYFA (SEQ ID NO:12)
in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid.
3. (currently amended) The PARP homolog as claimed in claim 1 , ~~further~~ comprising the sequence:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15)

in which the X radicals are, independently of one another, any amino acid.

4-32. (canceled)

33. (previously presented) The PARP homolog as claimed in claim 1, wherein the functional NAD⁺ binding domain comprises the following sequence:

LLWHG(S/T)X₇IL(S/T)XGLR(I/V)XPX_n(S/T)GX₃GKGIYFAX₃SKSAXY (SEQ ID NO:13)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

34. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising sequence:

AX₃FXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16)

in which the X radicals are, independently of one another, any amino acid.

35. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising sequence:

XL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17)

in which the X radicals are, independently of one another, any amino acid.

36. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising sequence:

FYTXIPHXFGX₃PP (SEQ ID NO:18)

in which the X radicals are, independently of one another, any amino acid.

37. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising sequence:

KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

38. (currently amended) An isolated poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) ~~or a functional equivalent thereof which is at least 95% homologous to~~ or a PARP homolog having at least 85% identity with human PARP2 (SEQ ID NO: 2), which exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

- a) has a functional NAD⁺ binding domain comprising the sequence

PX_n(S/T)GX₃GKGIYFA (SEQ ID NO:11)

in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

and

- b) lacks a zinc finger sequence of the formula

CX₂CX_mHX₂C (SEQ ID NO:30)

in which m is an integral value of 28 or 30, and the X radicals are, independently of one another, any amino acid

further comprising a leucine zipper-like sequence:

(L/V)X₆LX₆LX₆L (SEQ ID NO: 14)

wherein X radicals are, independently of one another, any amino acid.

39. (currently amended) The PARP homolog as claimed in claim 38, ~~further~~ comprising at least one of the following sequences:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15),

AX₃FXXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),

QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),

FYTXIPHFXFGX₃PP (SEQ ID NO:18), and

KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

40. (currently amended) The PARP homolog as claimed in claim 38, ~~further~~ comprising sequences:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15)
AX₃FXX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),
QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),
FYTXIPHXXFGX₃PP (SEQ ID NO:18), and
KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

41. (currently amended) The PARP homolog as claimed in claim 38, ~~further~~ comprising sequences:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15)
AX₃FXX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),
QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),
FYTXIPHXXFGX₃PP (SEQ ID NO:18), and
KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO:15)

is closest to the N terminus.

42. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising sequences:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15)
AX₃FXX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),
QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),
FYTXIPHXXFGX₃PP (SEQ ID NO:18), and
KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid.

43. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising sequences:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15)

AX₃FXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),

QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),

FYTXIPHXFGX₃PP (SEQ ID NO:18), and

KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO:15)

is closest to the N terminus.

44. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising at least one of the following:

GX₃LXEVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YXYX₃QXYLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

45. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising

GX₃LXEVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

46. (currently amended) The PARP homolog as claimed in claim 1, ~~further~~ comprising

GX₃LXEVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid, wherein

$E(Y/F)X_2YX_3QX_4YLL$ (SEQ ID NO: 22)

is closest to the C terminus.

47. (currently amended) An isolated poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2) ~~or a functional equivalent thereof which is at least 95% homologous to~~ or a PARP homologue having at least 85% identity with human PARP2 (SEQ ID NO: 2), which exhibits poly(ADP-ribose)-synthesizing activity, and has an amino acid sequence which

a) has a functional NAD^+ binding domain comprising the sequence

$PX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:11)

in which n is an integral value from 1 to 5, and the X radicals are, independently of one another, any amino acid;

and

b) lacks a zinc finger sequence.

48. (previously presented) The PARP homolog as claimed in claim 47, wherein said PARP lacks a zinc finger sequence of the formula

$CX_2CX_mHX_2C$ (SEQ ID NO:30)

in which m is an integral value of 28 or 30, and

the X radicals are, independently of one another, any amino acid.

49. (previously presented) The PARP homolog as claimed in claim 47, wherein the functional NAD^+ binding domain comprises the following sequence:

$(S/T)XGLR(I/V)XPX_n(S/T)GX_3GKGIYFA$ (SEQ ID NO:12)

in which n is an integral value from 1 to 5, and

the X radicals are, independently of one another, any amino acid.

50. (previously presented) The PARP homolog as claimed in claim 47, wherein the functional NAD⁺ binding domain comprises the following sequence:
LLWHG(S/T)X₇IL(S/T)XGLR(I/V)XPX_n(S/T)GX₃GKGIYFAX₃SKSAXY (SEQ ID NO:13)
in which n is an integral value from 1 to 5, and
the X radicals are, independently of one another, any amino acid.
51. (currently amended) The PARP homolog as claimed in claim 47, further comprising a leucine zipper-like sequence:
(L/V)X₆LX₆LX₆L (SEQ ID NO: 14)
wherein X radicals are, independently of one another, any amino acid.
52. (currently amended) The PARP homolog as claimed in claim 51, further comprising at least one of the following sequences:
LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15),
AX₃FXXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),
QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),
FYTXIPHXFGX₃PP (SEQ ID NO:18), and
KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)
in which the X radicals are, independently of one another, any amino acid.
53. (currently amended) The PARP homolog as claimed in claim 51, further comprising:
LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15),
AX₃FXXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),
QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),
FYTXIPHXFGX₃PP (SEQ ID NO:18), and
KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)
in which the X radicals are, independently of one another, any amino acid.

54. (currently amended) The PARP homolog as claimed in claim 51, ~~further~~ comprising:

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15),
AX₃FXKX₄KTXNXWX₅FX₃PXK (SEQ ID NO:16),
QXL(I/L)X₂IX₉MX₁₀PLGKLX₃QIX₆L (SEQ ID NO:17),
FYTXIPHXFGX₃PP (SEQ ID NO:18), and
KX₃LX₂LXDIEXAX₂L (SEQ ID NO:19)

in which the X radicals are, independently of one another, any amino acid, wherein

LX₉NX₂YX₂QLLX(D/E)X_{10/11}WGRVG (SEQ ID NO: 15)

is closest to the N terminus.

55. (currently amended) The PARP homolog as claimed in claim 47, ~~further~~ comprising at least one of the following:

GX₃LXEVALG (SEQ ID NO: 20),
GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and
E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

56. (currently amended) The PARP homolog as claimed in claim 47, ~~further~~ comprising

GX₃LXEVALG (SEQ ID NO: 20),
GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and
E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

57. (currently amended) The PARP homolog as claimed in claim 47, ~~further~~ comprising

GX₃LXEVALG (SEQ ID NO: 20),
GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid, wherein

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

is closest to the C terminus.

58. (currently amended) The PARP homolog as claimed in claim 51, ~~further~~ comprising at least one of the following:

GX₃LXVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

59. (currently amended) The PARP homolog as claimed in claim 51, ~~further~~ comprising

GX₃LXEVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid.

60. (currently amended) The PARP homolog as claimed in claim 51, ~~further~~ comprising

GX₃LXEVALG (SEQ ID NO: 20),

GX₂SX₄GX₃PX_aLXGX₂V (SEQ ID NO: 21), and

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

in which a is 7 to 9 and

X is any amino acid, wherein

E(Y/F)X₂YX₃QX₄YLL (SEQ ID NO: 22)

is closest to the C terminus.

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61. (new) An isolated and purified-poly(ADP-ribose) polymerase (PARP) homolog comprising human PARP2 (SEQ ID NO: 2).